



Genomics and Proteomics: Diagnosis and Treatment Applications in Brain Trauma

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Genomics:

In the past several years, our studies have documented changes in targeted or selected genes following brain injury using QRT-PCR. Although this approach is critical and hypothesis driven, it does not allow broad and detailed assessments of changes in the expression of various gene families following insults to the brain.

Recent developments in genomics with the availability of smaller and specific functional DNA microarray chips inspired us to initiate studies in this research arena.





QRT/PCR versus Microarray

QRT/PCR: Precise and accurate measure of mRNA of a single gene at a time. Not suitable for rapid and quick screening of large number of gene families.

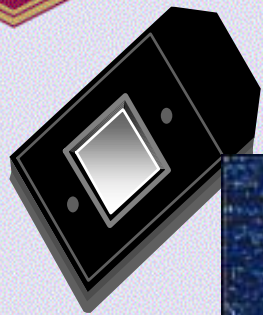
Microarray: Suitable for rapid and quick screening of large number of gene families. Yield only qualitative changes of gene expression and is not always accurate. Needs additional confirmation by QRT/PCR





Affymetrix® Rat Neurobiology Chip

(2500 gene probes with 1320 functional gene probes)



GeneChip® Probe Array

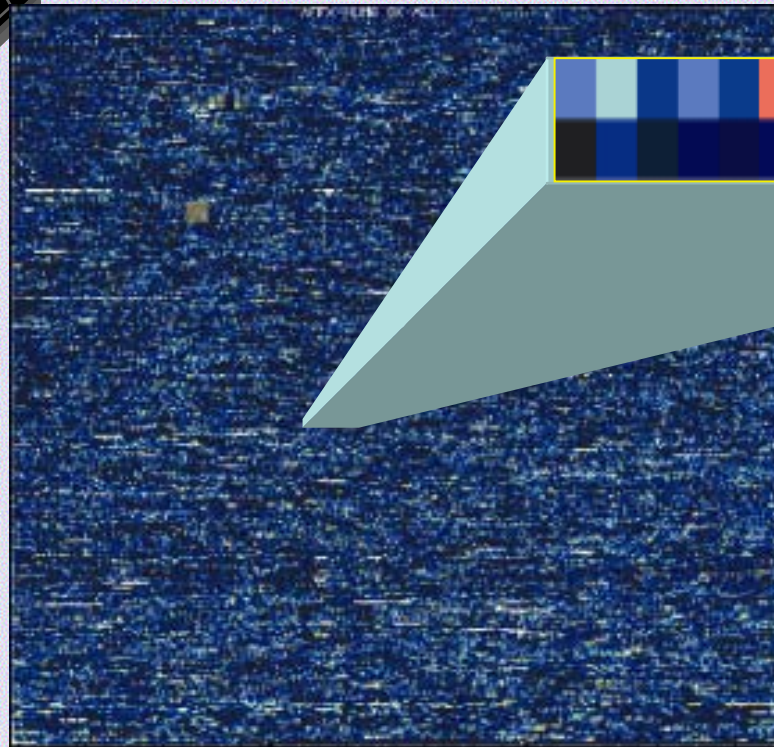


Image of Hybridized Probe Array

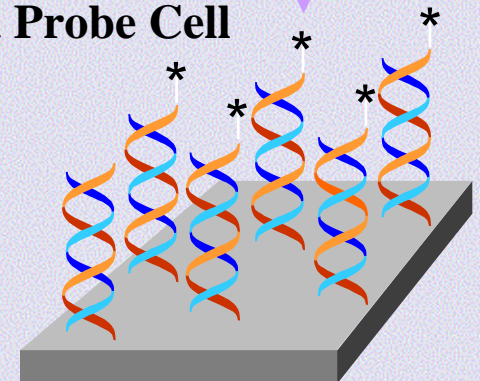
Probe Set



Probe Pair

PM
MM

Hybridized Probe Cell



Probe Cell
(feature)

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Gene Function

Up

Down

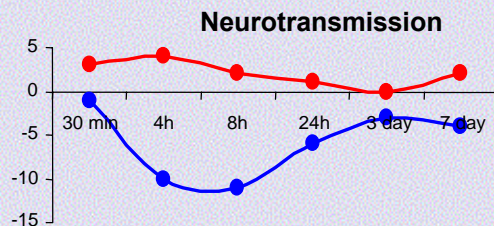
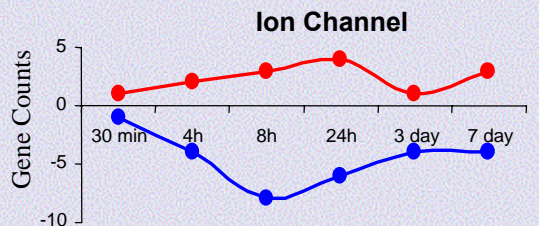
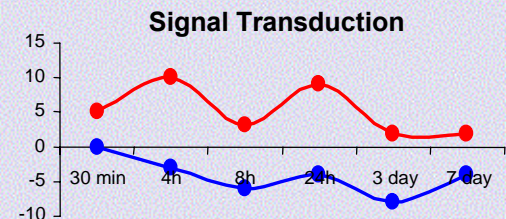
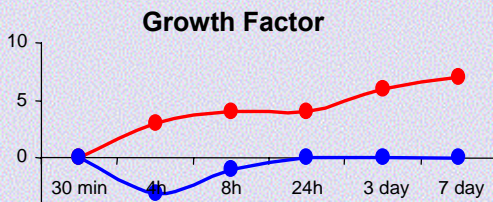
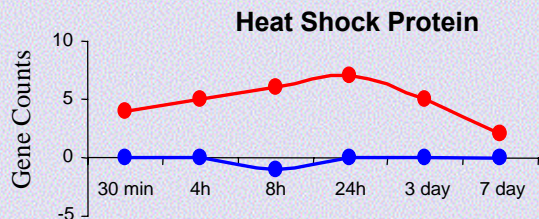
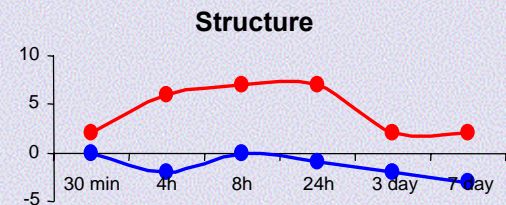
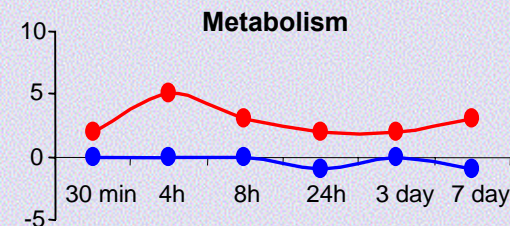
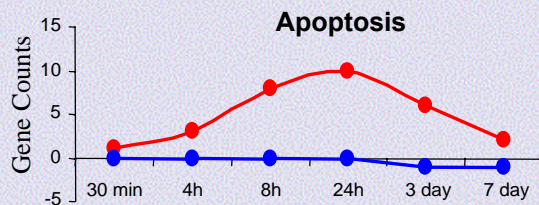
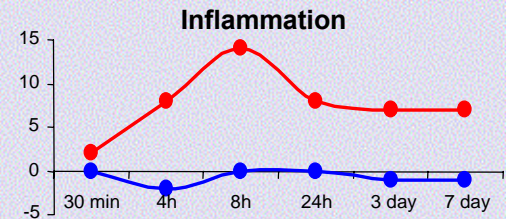
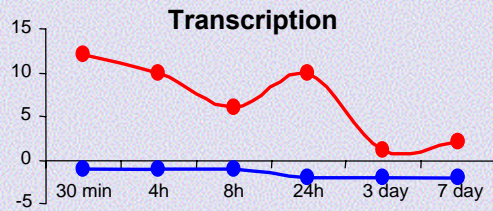
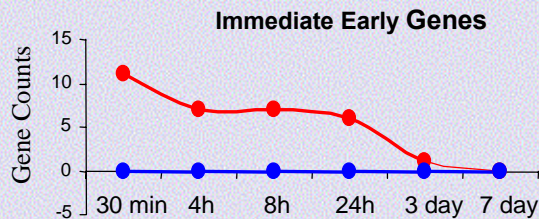
(Following
Brain injury)

Inflammation	20	3
Immediately early gene	17	0
Apoptosis	17	1
Growth Factor	17	2
Structure	17	6
Transcription	15	3
Metabolism	13	7
Heat Shock Protein	8	1
Signal transduction	19	20
Ion channels	14	22
Neurotransmission/release	7	26
Miscellaneous	14	15
Total (284)	178	106





Temporal Profile of Genomic Response after Ischemic Brain Injury



● Up-Regulated Gene Counts
● Down-Regulated Gene Counts

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Apoptosis

Gene Name	30 min	4 h	8 h	24 h	3 day	7 day
Bcl-x β	3.4	4.5	5.6	3.8		
DP5		2.8	4.0			
Fas antigen ligand		4.1	4.4	6.1		
inhibitor of apoptosis p			2.6	3.0		
Bcl-2			3.0			
calpain large subunit (nCL-4)			4.6	3.9		
casepase 2			5.2			
caspase-7			3.2	5.5		
p94 (calpain 3) p				2.6		
IL-1 β CE related p				3.1		
IL-1 β CE				2.6	3.8	
rBax α				3.8	3.0	
IGIF isoform α prec.					6.3	
SP120,					2.3	
Nedd2/Ich-1					5.6	7.9
nuclear oncoprotein p53					10.9	5.4
calpain isoform Lp85						3.9





Proteomics:

A powerful research tool that extends our molecular evaluations beyond ‘genomics’ in that it can not only identify up- or down-regulation of functional proteins, but can also identify specific protein modifications (e.g. phosphorylation, methylation, truncation etc) following an insult.





Ultimate goals of our studies:

- ❖ Identify protein changes specific to the brain injury, and correlate these changes in CSF & plasma for development of possible biomarkers.
- ❖ Use the proteomics information to develop a “diagnostic biomarker capability” to identify not only the severity but also anatomical extent of injury.
- ❖ Develop therapeutic interventions based on changes in specific protein families.

Although these are very ambitious goals, but are achievable by extensive studies.





Why study the Proteome?

Genome: The blue-print plan for Man

Proteome: The parts-list for Man

All of the cell's working parts are proteins



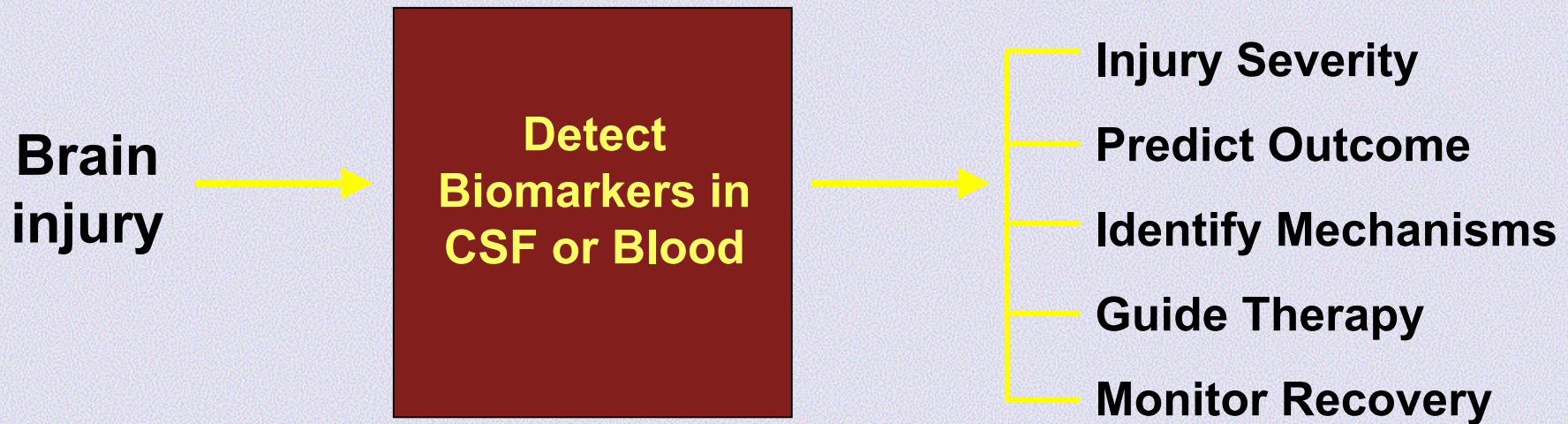


Bio-Markers of Brain Injury

- **Biomarkers**

- measurable internal indicators of changes in organisms at the molecular or cellular level

Develop biomarkers that can be measured in blood or CSF





Classical Proteomics

Separation of proteins →
2D gel electrophoresis

Characterization of proteins →
Mass spectrometry





Similar to our collaborative efforts with Dr. Maryanne Vahey (WRAIR-Microarray core facility, Rockville), we have established a proteomics collaboration with Dr. Ronald Hayes (McKnight Foundation, University of Florida) and initiated a comprehensive, time-dependent analysis of proteomic changes in brain, CSF and plasma following ischemic and traumatic experimental brain injury.





Participants

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